0420  0590
/0330  0928  0420/  OIPE
#5

RAW SEQUENCE LISTING                    DATE: 10/01/2001
PATENT APPLICATION:  US/09/732,436B      TIME: 13:56:35

       Input Set : A:\Cura-111.app
       Output Set: N:\CRF3\10012001\I732436B.raw

 3  <110> APPLICANT: Prayaga, Suhhirdas K
 4         Shimkets, Richard A
 6  <120> TITLE OF INVENTION: Novel Polypeptides and Polynucleotides Encoding Same
 8  <130> FILE REFERENCE: 15966-615
10  <140> CURRENT APPLICATION NUMBER: 09/732,436B
11  <141> CURRENT FILING DATE: 2000-12-07
13  <150> PRIOR APPLICATION NUMBER: 60/169,887
14  <151> PRIOR FILING DATE: 1999-12-09
16  <150> PRIOR APPLICATION NUMBER: 60/170,230
17  <151> PRIOR FILING DATE: 1999-12-10
19  <160> NUMBER OF SEQ ID NOS: 26
21  <170> SOFTWARE: PatentIn Ver. 2.1
23  <210> SEQ ID NO: 1
24  <211> LENGTH: 475
25  <212> TYPE: DNA
26  <213> ORGANISM: Homo sapiens
28  <400> SEQUENCE: 1
29  accaatggtc tccttgctgg tggcattggt gatgatctcc tgccacatct attccctttt 60
30  ctgcgacctg cctaaagctc aggtgatttc tgccctccat aagatgcacc agcagatctt 120
31  cagcctcttt ttacacaagg gcttgtctga tgcttggaat agggccttcc tggacaaact 180
32  ccagactgga tttcatcagc agctggaaga cctggagacc tgctttggta tagaggatgg 240
33  gaagcaagag tctgccctgg aaattgaggg ccctacactg gccataaaga ggtacttcca 300
34  gggagtacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgtcgt 360
35  aatggtaaag ggatttttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420
36  gaactgcaaa aaaaatctgg aaaaggtaat ctatttagca gaagagtgaa agctg      475
39  <210> SEQ ID NO: 2
40  <211> LENGTH: 154
41  <212> TYPE: PRT
42  <213> ORGANISM: Homo sapiens
44  <400> SEQUENCE: 2
45  Met Val Ser Leu Leu Val Ala Leu Val Met Ile Ser Cys His Ile Tyr
46   1               5                  10                  15
48  Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His
49              20                  25                  30
51  Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
52           35                  40                  45
54  Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
55        50                  55                  60
57  Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys
58   65                  70                  75                  80
60  Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg
61              85                  90                  95
63  Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn
64             100                 105                 110
66  Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr
67             115                 120                 125
69  Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn

RAW SEQUENCE LISTING          DATE: 10/01/2001
PATENT APPLICATION:  US/09/732,436B     TIME: 13:56:35

Input Set : A:\Cura-111.app
Output Set: N:\CRF3\10012001\I732436B.raw

```
     70      130                     135                     140
     72 Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu
     73 145                 150
     76 <210> SEQ ID NO: 3
     77 <211> LENGTH: 610
     78 <212> TYPE: DNA
     79 <213> ORGANISM: Homo sapiens
     81 <220> FEATURE:
     82 <221> NAME/KEY: misc_feature
     83 <222> LOCATION: (74)..(208)
     84 <223> OTHER INFORMATION: Wherein n is a or t or c or g.
     86 <400> SEQUENCE: 3
     87 accaatggtc tccttgctgg tggcattggt gatgatctcc tgccacatct attcccttt  60
W--> 88 ctgcgacctg cctnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
W--> 89 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180  or
W--> 90 nnnnnnnnnn nnnnnnnnnn nnnnnnnnaa agctcaggtg atttctgccc tccataagat 240
     91 gcaccagcag atcttcagcc tctttttaca caagggcttg tctgatgctt ggaatagggc 300
     92 cttcctggac aaactccaga ctggatttca tcagcagctg gaagacctgg agacctgctt 360
     93 tggtatagag gatgggaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420
     94 aaagaggtac ttccagggag tacatttctt cttgaaagag aggaaattca ggaactgtac 480
     95 ctgggaggtt gtcgtaatgg taaagggatt tttcttaagc acaaaacttc aagaaaaaga 540
     96 gaacagaaga aaagagaact gcaaaaaaaa tctggaaaag gtaatctatt tagcagaaga 600
     97 gtgaaagctg                                                     610
    100 <210> SEQ ID NO: 4
    101 <211> LENGTH: 199
    102 <212> TYPE: PRT
    103 <213> ORGANISM: Homo sapiens
    105 <220> FEATURE:
    106 <221> NAME/KEY: VARIANT
    107 <222> LOCATION: (24)..(68)
    108 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
    110 <400> SEQUENCE: 4
    111 Met Val Ser Leu Leu Val Ala Leu Val Met Ile Ser Cys His Ile Tyr
    112   1               5               10                  15
W--> 114 Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    115             20              25                  30
W--> 117 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    118         35              40                  45
W--> 120 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    121     50              55                  60
W--> 123 Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His
    124 65              70                  75                  80
    126 Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp
    127             85              90                  95
    129 Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu
    130             100             105                 110
    132 Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser
    133         115             120                 125
    135 Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln
```

```
136    130                    135                140
138 Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp
139 145              150                155                160
141 Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln
142              165                170                175
144 Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys
145              180              185                190
147 Val Ile Tyr Leu Ala Glu Glu
148        195
151 <210> SEQ ID NO: 5
152 <211> LENGTH: 1887
153 <212> TYPE: DNA
154 <213> ORGANISM: Homo sapiens
156 <400> SEQUENCE: 5
157 atggccatcc tcccgttgct cctgtgcctg ctgccgctgg cccctgcctc atccccaccc 60
158 cagtcagcca cacccagccc atgtccccgc cgctgccgct gccagacaca gtcgctgccc 120
159 ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgccgg 180
160 gcagccgagc tgcggctggc agacaacttc atcgcctccg tgcgccgccg cgacctggcc 240
161 aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
162 ggcgccttcg ccgacctgcg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
163 tcactgggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
164 aaccagctgg cagcgctggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
165 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggccctggg ccgcctgggc 540
166 aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgcccgc cggcgctttt 600
167 tcccgcctgc acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660
168 cccgacccac tcttctcccg cctgcccctg ctcgccaggc cccggggctc gcccgcctct 720
169 gccctggtgc tggcctttgg cgggaacccc ctgcactgca actgcgagct ggtgtggctg 780
170 cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt ccccacctgc tctgggcggc 840
171 cgctacttct gggcggtggg cgaggaggag tttgtctgcg agccgcccgt ggtgactcac 900
172 cgctcaccac ctctggctgt gcccgcaggt cggccggctg ccctgcgctg ccgggcagtg 960
173 ggggacccag agccccgtgt gcgttgggtg tcaccccagg gccggctgct aggcaactca 1020
174 agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080
175 ggtggcatct tcacctgcat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
176 ctgactgtgg gtcccccacc acctcctcag ctagccaaca gcaccagctg tgaccccccg 1200
177 cgggacgggg atcctgatgc tctcaccccca ccctccgctg cctctgcttc tgccaaggtg 1260
178 gccgacactg ggcccccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320
179 gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380
180 tacaacagct cggctgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440
181 ttcctgctga cggacctggc gtcaggccgg acctacgatc tgtgcgtgct cgccgtgtat 1500
182 gaggacagcg ccacgggggct cacggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
183 gaacctgcgc tgcggccatg cggggcgccg cacgctccct tcctgggcgg cacgatgatc 1620
184 atcgcgctgg cggcgtcat cgtagcctcg gtactggtct tcatcttcgt gctgctaatg 1680
185 cgctacaagg tgcacggcgg ccagcccccc ggcaaggcca agattcccgc gcctgttagc 1740
186 agcgtttgct cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccgcc 1800
187 ccggagcccg cggcgctcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860
188 cccggccacg aacctgtggg accctag 1887
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 628
193 <212> TYPE: PRT
```

```
194 <213> ORGANISM: Homo sapiens
196 <400> SEQUENCE: 6
197 Met Ala Ile Leu Pro Leu Leu Leu Cys Leu Leu Pro Leu Ala Pro Ala
198   1                   5                  10                  15
200 Ser Ser Pro Pro Gln Ser Ala Thr Pro Ser Pro Cys Pro Arg Arg Cys
201              20                  25                  30
203 Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala
204          35                  40                  45
206 Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu
207       50                  55                  60
209 Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala
210   65                  70                  75                  80
212 Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg
213                  85                  90                  95
215 His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu
216             100                 105                 110
218 His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg
219             115                 120                 125
221 Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala
222       130                 135                 140
224 Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp
225 145                 150                 155                 160
227 Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu
228                 165                 170                 175
230 Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu
231             180                 185                 190
233 Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg
234             195                 200                 205
236 Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu
237       210                 215                 220
239 Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser
240 225                 230                 235                 240
242 Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu
243                 245                 250                 255
245 Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys
246             260                 265                 270
248 Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu
249             275                 280                 285
251 Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro
252       290                 295                 300
254 Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val
255 305                 310                 315                 320
257 Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu
258             325                 330                 335
260 Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu
261             340                 345                 350
263 Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala
264       355                 360                 365
266 Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly
```

```
267      370                   375                   380
269 Pro Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro
270 385                   390                   395                   400
272 Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala
273                   405                   410                   415
275 Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln
276                   420                   425                   430
278 Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln
279             435                   440                   445
281 Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser
282       450                   455                   460
284 Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser
285 465                   470                   475                   480
287 Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val
288                   485                   490                   495
290 Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
291                   500                   505                   510
293 Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
294             515                   520                   525
296 Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
297       530                   535                   540
299 Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
300 545                   550                   555                   560
302 Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
303             565                   570                   575
305 Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
306             580                   585                   590
308 Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
309       595                   600                   605
311 His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
312       610                   615                   620
314 Pro Val Gly Pro
315 625
318 <210> SEQ ID NO: 7
319 <211> LENGTH: 802
320 <212> TYPE: DNA
321 <213> ORGANISM: Equus caballus
323 <400> SEQUENCE: 7
324 aaatcagaga tattataagt acacatatcc ctattaacgg cctagttggc aagaatgtca 60
325 tcagagaacc tcggtccaag ttcagagaca cccagctcag ccaggccagc agcaccctcg 120
326 ttttccccat ggccctcctg ccctctctct tgacggccct ggtggtgtac gagttatggc 180
327 cctgtggagc tctgggctgt gacctgcctc agaaccacat cctggttagc aggaagaact 240
328 tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaag 300
329 acttcaggtt cccccaggac atggcggatg gcaggcagtt cccagaggcc aggccgcgt 360
330 ctgtcctcca cgagatgctc cagcagatct tcagcctctt ccacacagag cgctcgtctg 420
331 ctgcctggaa cacgaccctc ctggacgaac tctgcacggg actccttcgg cagctggaag 480
332 acctggacac ctgtttggag caggagatgg gagaggaaga atctgccctg ggaactgtgc 540
333 gccctacact ggccgtgaag aggtacttcc ggggggatcca tctctacctg aaagagaaga 600
334 aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctcttcat 660
```

VERIFICATION SUMMARY                    DATE: 10/01/2001
PATENT APPLICATION:   US/09/732,436B    TIME: 13:56:36

Input Set  : A:\Cura-111.app
Output Set: N:\CRF3\10012001\I732436B.raw

```
L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
```